

flower drop in response to several concentrations of ethylene (0, 0.1, 0.2, 0.5, 1 and 2 $\mu\text{l l}^{-1}$) over 96 h. High concentrations (0.5–2 $\mu\text{l l}^{-1}$) promoted abscission of open and unopened flowers, while lower concentrations (0.1–0.2 $\mu\text{l l}^{-1}$) induced abscission of unopened buds preferentially. Subsequent experiments examined soluble carbohydrate levels (by gas chromatography) and flower abscission in plants under simulated display (fluorescent lights) or transport (dark) conditions with or without continuous 1-methylcyclopropene (1-MCP, 0.1 $\mu\text{l l}^{-1}$) for 96 h. Under fluorescent lights, glucose and fructose levels declined after 24 h and then remained steady, but abscission was only observed after 72 and 96 h. In contrast, glucose and fructose levels of plants kept in the dark increased after 24 h, but by 96 h had returned to the same level as plants kept under fluorescent lights. Plants treated with 1-MCP were effectively protected from the effects of applied ethylene, exhibiting low levels of abscission. Soluble carbohydrate levels and flower abscission were also investigated in defoliated plants, the results of which will be discussed in the context of potential pathways of carbohydrate-induced abscission.

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Genomics of quantitative disease resistance in African maize varieties

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Maize is an important crop in Africa and one of the major food sources for southern and eastern Africa. The growth of maize by large-scale and developing farmers is hampered by disease losses, of which grey leaf spot (GLS), caused by the fungus *Cercospora zeina*, is one of the most severe. Deployment of quantitative disease resistance to GLS in the wide range of maize varieties that are required for the many agro-ecological zones in Southern Africa remains the most desirable solution. This work, a collaborative project between the University of Pretoria, the Centre for Genomic and Proteomic Research, the African Centre for Crop Improvement and PANNAR Research Services (Pty.) Ltd., is sponsored by PlantBio and is the first of its kind in SA. The project aim is to identify the genes involved in quantitative resistance to *C. zeina*. The approach is to combine conventional analysis of resistance quantitative trait loci (QTL) with identification of

expression QTL (eQTL), where expression of each gene in *C. zeina*-infected maize plants (as determined by microarray analysis) is treated as a quantitative trait and QTL controlling gene expression are identified in a segregating population. The eQTL method will be discussed in addition to up-to-date progress in the project.

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Changes in peroxidase and phenylalanine ammonia-lyase activities of white clover (*Trifolium repens* L. cv. Regal) biotypes in response to ozone treatment

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Increases in industrialization have resulted in increases of harmful air pollution gasses. Ozone was identified as one of the gasses that pose serious problems to the agricultural industry. Ozone enters the plant through the stomata where after it dissolves to form oxygen radicals. These radicals have the ability to disrupt cellular processes. The ability of a plant to scavenge these elevated levels of radicals is a key step in the defence mechanism of plants. The effect of ozone on the antioxidant defence mechanism of two white clover (*Trifolium repens* L. cv. Regal) biotypes (ozone sensitive and ozone resistant) was investigated. The clover plants were exposed to 80 ppb ozone for 28 days, 7 h/day. Open top chambers were used to fumigate the clover. The activities of peroxidases and phenylalanine ammonia-lyase were spectrophotometrically determined. Both susceptible and resistant plants showed increases in peroxidase and phenylalanine ammonia-lyase activities, but the increase in the resistant plants was superior. These results indicate that the antioxidant defence mechanism has an important task in the defence mechanism of white clover to ozone.

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New generic circumscriptions in the tribe Crotalariaeae (Fabaceae)

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The tribe Crotalariaeae is a large and diverse group of papilionoid legumes that are sub-endemic to Africa. A phylogenetic

study of all 11 genera of the tribe with a representative sample of 117 species was undertaken, based on molecular (nrITS and *rbcL*) and morphological data. This showed the Crotalariaeae to be strongly supported as monophyletic and sister to the tribe Genisteae. The genera *Lebeckia*, *Lotononis* and *Wiborgia*, as currently circumscribed, are paraphyletic. Molecular, morphological and anatomical data support new generic classification systems for both *Lebeckia* and *Lotononis*. *Lebeckia* s.l. is split into three genera, viz. *Lebeckia* s.s. (*L.* sect. *Lebeckia*), *Calobota* (*L.* sect. *Calobota*, *L.* sect. *Stiza* and the monotypic genus *Spartidium*) and a new genus “*Wiborgiella*” (*L.* sect. *Viborgioides*, *L. inflata*, *L. mucronata* and *Wiborgia humilis*). The new classification is supported by morphological characters such as the habit, bark formation on twigs, leaf type, leaf anatomy and anther configuration. The results also show that *Lotononis* s.l. actually comprises five monophyletic genera, viz. *Lotononis* s.s. (*L.* section *Lotononis* and allies), *Leobordea* (*L.* section *Leobordea* and allies), *Listia* (*L.* section *Listia*), *Euchlora* (*L.* section *Euchlora*) and “*Ezoloba*” (a new, as yet undescribed, monotypic genus comprising the anomalous *L. macrocarpa*). These genera can be recognized by a combination of habit, leaf and stipule morphology, anther configuration, pod morphology, chromosome number and the presence or absence of pyrrolizidine alkaloids, quinolizidine alkaloids and cyanogenic glucosides. When these changes are taken into consideration, the total number of genera in the tribe Crotalariaeae increases to 16. This presentation will focus on the changes at generic level and the three major lineages within the Crotalariaeae as revealed by this study, namely the “Cape”, *Lotononis* and *Crotalaria* groups. The tribe Crotalariaeae is a complicated group that shows extensive convergence in several characters. As a result, the generic delimitations are based mainly on the profound insights obtained by several students of this group over many years of dedicated study. The molecular results now add an important new dimension to our understanding of relationships and generic delimitations.

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Do soil nutrients determine the distribution of vegetation?

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Soil nutrient status is often correlated with vegetation pattern. The correlations are often assumed to be causal so that soil nutrients are thought to account for major biome distribution. For example, the Brazilian cerrado, South American savanna, occurs on nutrient poor soils which many authors have argued are too poor in nutrients to support forests. I briefly review evidence for and against the importance of low nutrients (especially phosphorus) in controlling the distribution of vegetation. Evidence from invasives, in particular, suggests that nutrient constraints on major vegetation patterns are far less

than is widely believed. Soil nutrient hypotheses of vegetation distribution need much more rigorous testing to better understand the role of soil nutrients in limiting future global vegetation change.

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Loss of functionality during aphid infestation: Causes and effects on transport systems in leaves

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Feeding damage caused by the Russian wheat aphid RWA, biotype SA1, *Diuraphis noxia* Mordvilko on leaf blades of susceptible and resistant wheat cultivars (*Triticum aestivum* L. var. Betta and Betta-Dn1 respectively) is limited in Betta-Dn1, compared with Betta. Limitation of damage in the resistant cultivar is in part ascribed to the resistance gene, Dn-1. However, South Africa now faces a potentially serious threat to grain production, with the appearance of a more virulent biotype, RWA SA-2, which is apparently unaffected by the Sn-1 resistance gene. TEM studies reveal that mesophyll tissues in resistant and susceptible lines are compromised and show increased damage at the cellular (including cell wall), sub-cellular (plasma membrane and endomembrane complexes), as well as at the organelle (chloroplast and mitochondrial) levels. Probes result in extensive saliva deposition and massive wound callose formation. This study revealed that the resistant line initially sustains limited damage, but prolonged feeding invariably causes severe damage to the vascular system. Water exits xylem to satisfy the requirements of transpiration, osmotic balance and cell-to-cell transport of assimilates. The exchange pathway from the xylem to the phloem as well as to the mesophyll is compromised as a result of the infrequent stops made by the aphids to drink water, which is always preceded by blowing debris and salivary material out of the aphid stylet feeding canals. TEM studies show that this watery saliva diffuses through the xylem vessels crosses the pit membrane, but does not cross the plasma membrane on the xylem parenchyma cell side. Salivary deposition prevents exchange from the xylem across the parenchyma interface. Given the complexity of the exchange pathway from xylem to parenchyma and the known endocytotic process that occur there, we suspect that the retrieval and transport pathways at this interface, are compromised. This paper reviews the effects of RWA SA-1 and SA-2 probing and feeding on the structural and physiological integrity of the leaf vascular system and explores the potential damage caused by saliva to the xylem to phloem retrieval system.

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